

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: February 13, 2002, 10:08:42 ; Search time 23.07 Seconds  
(without alignments)  
120.467 Million cell updates/sec

Perfect score: 51

Sequence: 1 XCXXXXCXXXXCXXXXCXX 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_17:  
1: sp\_archae:/\*  
2: sp\_bacteria:/\*  
3: sp\_fungi:/\*  
4: sp\_human:/\*  
5: sp\_invertebrate:/\*  
6: sp\_mammal:/\*  
7: sp\_minc:/\*  
8: sp\_organelle:/\*  
9: sp\_phage:/\*  
10: sp\_plant:/\*  
11: sp\_rodent:/\*  
12: sp\_virus:/\*  
13: sp\_vertibrate:/\*  
14: sp\_unclassified:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	29	56.9	117	10 Q40229	Q40229 lilium long
2	28	54.9	243	2 Q9RZ25	Q9rz25 deinococcus
3	28	54.9	244	10 Q9S0J9	Q9s0J9 arabidopsis
4	28	54.9	454	10 Q9Af61	Q9Af61 triticum ae
5	28	54.9	462	10 Q39249	Q39249 arabidopsis
6	28	54.9	472	10 Q9SM43	Q9SM43 spinacia ol
7	28	54.9	473	10 Q40231	Q40231 lactuca sat
8	28	54.9	478	10 Q40593	Q40593 nicotiana t
9	28	54.9	776	2 Q47412	Q47412 escherichia
10	28	54.9	1297	5 Q9U350	Q9U350 caenorhabdi
11	28	54.9	2948	5 Q93785	Q93785 caenorhabdi
12	27	52.9	99	5 Q9N329	Q9N329 caenorhabdi
13	27	52.9	233	5 Q9NJ95	Q9nj95 caenorhabdi
14	27	52.9	428	11 Q9D617	Q9d617 mus musculu
15	27	52.9	441	5 Q9W5XL	Q9w5xl drosophila
16	27	52.9	565	10 Q9M195	Q9m195 arabidopsis
17	27	52.9	568	5 Q9N195	Q9n195 caenorhabdi
18	27	52.9	580	5 Q9VM37	Q9vm37 drosophila
19	27	52.9	2146	5 Q9VC97	Q9vc97 drosophila

Query Match 8  
Best Local Similarity 56.9%; Score 29; DB 10; Length 117;

Best Local Similarity 23.5%; Pred. No. 2,4;  
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=CV. HINOMOTO; TISSUE=FLORAL BUD;  
RA Kobayashi T., Tabata S.;  
RL Submitted (DBC-1993) to the EMBL/GenBank/DBJ databases.  
RN [2]  
SEQUENCE FROM N.A.  
RC STRAIN=CV. HINOMOTO; TISSUE=FLORAL BUD;  
RA Kobayashi T., Tabata S.;  
RA Kobayashi E., Sato S., Hotta Y., Miyazima N., Tanaka A.,  
RA Tabata S.  
RT Characterization of cDNAs induced in meiotic prophase in lily  
RL DNA Res. 1:15-26(1994).  
DR EMBL; D21910; BAA0436.1;  
DR Mendel; 12768; Lillo; 1968; 12768.  
FT NON-TER 1  
SQ SEQUENCE 117 AA; 12625 MW; 972C71B1699CEA05 CRC64;

Query Match 2  
Best Local Similarity 56.9%; Score 29; DB 10; Length 117;  
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
Db 74 CTTSSKCKKGVTCSSKKC 18

RESULT	2	DR	PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
Q9RZ25	PRELIMINARY;	PRT;	243 AA.
ID	Q9RZ25;	PRT;	243 AA.
AC		PRT;	243 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	HYPOTHETICAL		
DE	26.2 KDA PROTEIN.		
GN	DRA0128.		
OS	Deinococcus radiodurans.		
OC	Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.		
OX	NCBI_TAXID=1299;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=RL;		
RX	MEDLINE=20036896; PubMed=10567266;		
RA	White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,		
RA	Gwyn M.L., Nelson W.C., Richardson D.L.,		
RA	Haft D.H., Gwyn M.L., Nelson W.C., Richardson D.L.,		
RA	Moffatt K.S., Qin H., Jiang L., Pauphile W., Crosby M.,		
RA	Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,		
RA	Markova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,		
RA	Ketchum K.A., Nelson K.E., Smith H.O., Venter J.C.,		
RA	Fraser C.M.;		
RT	"Genomic sequence of the radioresistant bacterium Deinococcus		
RT	radiodurans RL";		
DR	SCIENCE 286:1571-1577(1999).		
DR	EMBL; AEG01862; AAF12318.1; -.		
DR	TIGR; DRA0128; -.		
DR	InterPro; IPR001387; HTH_3.		
DR	InterPro; IPR000014; PAS.		
DR	Pfam; PF01388; HPH_3; 1.		
DR	SMART; SM00510; HTH_XRE; 1.		
DR	SMART; SM00051; PAS; 1.		
DR	Hypothetical Protein; Complete proteome.		
SQ	SEQUENCE 243 AA; 26235 MW; E5105B3C1859FEFE CRC64;		
Query Match	54.9%	Score	28; DB 2; Length 243;
Best Local Similarity	23.5%	Pred	No 4.8; Mismatches 0; Gaps 0;
Matches	4;	Conservative	0; Mismatches 13; Indels 0; Gaps 0;
QY	2 CXXXXCXXXXCXXXC 18		
Db	214 CRNHSACRDARTCSRK 230		
RESULT	3	DR	PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
Q9SJ09	PRELIMINARY;	PRT;	244 AA.
ID	Q9SJ09;	PRT;	244 AA.
AC		PRT;	244 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	T2767.23 (FRAGMENT).		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosidios II; Brassicaceae; Arabidopsis.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,		
RA	Kim C., Altai H., Bei Q., Chin C., Choi E., Conn L.,		
RA	Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,		
RA	Lenz C., Li J., Liu K., Liu K., Liu K., Mukharsky N., Nguyen M.,		
RA	Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,		
RA	Toriumi M., Vayshberg M., Yu G., Federeriel N.A., Theologis A.,		
RA	Ecker J.R.;		
RT	"Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome		
RT	I.";		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AC00632; AAF22898.1; -.		
DR	InterPro; IPR000566; Lipocln_cytFABP.		

RA	Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,	OX	NCBI_TaxID=4236;
RA	Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.	RN	[1]
RL		PP	SEQUENCE FROM N.A.
DR	U41133; AAC00321; -.	RC	STRAIN=ROMAINE;
DR	AC003981; AACF99753.1; -.	RX	MEDLINE=16270536; PubMed=8692813;
DR	6341; Arath; vail; 6341.	RA	Bugos R. C., Yamamoto H. Y.;
DR	InteroPro; IPR000566; Lipocin_cytFABP.	RT	"Molecular cloning of violaxanthin de-epoxidase from romaine lettuce and expression in Escherichia coli."
DR	PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.	RT	and expression in Escherichia coli."
KW	Signal.	RL	PROC. Natl. Acad. Sci. U.S.A. 93:6320-6325 (1996).
FT	SIGNAL 1 113 POTENTIAL.	DR	EMBL; U31462; AAC1937.1; -.
FT	CHAIN 114 462 VIOLAXANTHIN DE-EPOXIDASE.	DR	Mendel; 8691; Lacsas; Yeil; 691.
SEQUENCE	462 AA; 52017 MW; 58E37B2C12D426B CRC64;	DR	InterPro; IPR000566; Lipocin_cytFABP.
QY	2 CXXXXCXXXXCXXXC 18	DR	PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
Db	134 CIANPACAAANVACLQTC 150	KW	
Query Match	54.9%; Score 28; DB 10; Length 462;	FT	Transit peptide.
Best Local Similarity	23.5%; Pred. No. 5.1;	TRANSLIT	1 125 POTENTIAL.
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;		CHAIN	126 473 VIOLAXANTHIN DE-EPOXIDASE.
QY	2 CXXXXCXXXXCXXXC 18	SEQUENCE	473 AA; 54447 MW; 1B22522DC2C62699 CRC64;
RESULT	6	Query Match	54.9%; Score 28; DB 10; Length 473;
Q9SM43	PRELIMINARY;	Best Local Similarity	23.5%; Pred. No. 5.1;
ID	Q9SM43	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
AC		Query Match	54.9%; Score 28; DB 10; Length 473;
DT	01-MAY-2000 (TREMBLrel. 13, Created)	Best Local Similarity	23.5%; Pred. No. 5.1;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
DE	VIOLAXANTHIN DE-EPOXIDASE PRECURSOR.	Query Match	54.9%; Score 28; DB 10; Length 473;
GN		Best Local Similarity	23.5%; Pred. No. 5.1;
SVDEL		Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
OS	Spinacia oleracea (Spinach).	Query Match	54.9%; Score 28; DB 10; Length 473;
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Best Local Similarity	23.5%; Pred. No. 5.1;
OC	Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots;	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
OC	Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.	Query Match	54.9%; Score 28; DB 10; Length 473;
OX		Best Local Similarity	23.5%; Pred. No. 5.1;
NCBI_TaxID=562;		Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
RN		Query Match	54.9%; Score 28; DB 10; Length 473;
RP	SEQUENCE FROM N.A.	Best Local Similarity	23.5%; Pred. No. 5.1;
RC	TISSUE=LEAF;	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
RA	Emanuelsen A.K., Eskling M., Akerlund H.E.;	Query Match	54.9%; Score 28; DB 10; Length 473;
RT	"Cloning and sequencing of <i>Spinacia oleracea</i> violaxanthin de-	Best Local Similarity	23.5%; Pred. No. 5.1;
RT	epoxidase."	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.	Query Match	54.9%; Score 28; DB 10; Length 473;
DR	EMBL; AJ250433; CAB59211.1; -.	Best Local Similarity	23.5%; Pred. No. 5.1;
KW	Signal.	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
FT	SIGNAL 1 124 POTENTIAL.	Query Match	54.9%; Score 28; DB 10; Length 473;
FT	CHAIN 125 472 VIOLAXANTHIN DE-EPOXIDASE.	Best Local Similarity	23.5%; Pred. No. 5.1;
SEQUENCE	53658 MW; 12B4C8C69AB61E12 CRC64;	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
Db	145 CIANPACAAANVACLQTC 161	Query Match	54.9%; Score 28; DB 10; Length 473;
RESULT	7	Best Local Similarity	23.5%; Pred. No. 5.1;
Q40251	PRELIMINARY;	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
ID	Q40251;	Query Match	54.9%; Score 28; DB 10; Length 473;
AC	Q40251;	Best Local Similarity	23.5%; Pred. No. 5.1;
DT	01-NOV-1996 (TREMBLrel. 01, Created)	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	Query Match	54.9%; Score 28; DB 10; Length 473;
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	Best Local Similarity	23.5%; Pred. No. 5.1;
DE	VIOLAXANTHIN DE-EPOXIDASE PRECURSOR.	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
GN	VDE1.	Query Match	54.9%; Score 28; DB 10; Length 473;
OS	Lactuca sativa (Garden Lettuce).	Best Local Similarity	23.5%; Pred. No. 5.1;
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
OC	Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots;	Query Match	54.9%; Score 28; DB 10; Length 473;
OC	Asteridae; euasterids II; Asteraceae; Lactucae; Lactuca.	Best Local Similarity	23.5%; Pred. No. 5.1;
		Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	

DE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE B1 SUBUNIT ALPHA-PRIME-  
DE POLYPEPTIDE PRECURSOR.  
GN Escherichia coli.  
OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TAXID=562;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=84272624; PubMed=6087316;  
RA Carlson J., Fuchs J.A., Messing J.,  
RT Primary structure of the Escherichia coli ribonucleoside diphosphate  
reductase operon.;  
RT PROC. NATL. ACAD. SCI. U.S.A. 81:4294-4297(1984).  
RL DR CAH23569.1; -.  
DR HSSP; P00452; 5R1R.  
DR InterPro: IPR000788; Ribonucleo\_red.  
DR PF00317; ribonucleo\_red; 4.  
DR PRINTS; PRO1183; RIBODRASEM1.  
FT CHAIN 3 776 POTENTIAL.  
FT CHAIN 27 776 POTENTIAL.  
SEQUENCE 776 AA; 87626 MW; 152185957/CEC4CE6 CRC64;

Query Match 54.9%; Score 28; DB 2; Length 776;  
Best Local Similarity 23.5%; Pred. No. 5.4;  
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
RN [2]  
SEQUENCE FROM N.A.  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
AC Connell M., Cooper J., Coulson A.,  
RA Bonfield J., Burton J., Copsey T., Dear S., Du Z., Durbin R.,  
RA Craxton M., Dear S., Du Z., Fulton L., Gardner A.,  
RA Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Latrell N.,  
RA Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA McMurray A., Mortimore B., Shownkeen R.,  
RA Parsons J., Percy C., Raffkin L., Roopra A.,  
RA Smalton N., Smith A., Sonnhammer E., Staden R.,  
RA Thierry-Mieg J., Thomas K., Vaughan K.,  
RA Watson A., Weinstock L., Wilkins-Sprott J., Wohldman P.;  
RT a 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RN [3]  
SEQUENCE FROM N.A.  
RX MEDLINE=9065613; PubMed=9851916;  
RA none;  
RT \*Genome sequence of the nematode *C.elegans*: A platform for  
investigating biology";  
RL SCIENCE 282:2012-2018(1998).  
CC -1- SIMILARITY: TO PANCREATIC TRYPSIN INHIBITOR (KUNITZ) DOMAIN.  
DR EMBL; Z81138; CAB53320 1; -.  
DR HSSP; P31713; 1SHP.  
DR InterPro: IPR00289; EB.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR PF01683; EB; 2.  
DR Pfam; PF00114; Kunitz\_BPTI; 6.  
DR PRINTS; PRO00739; BASICPIASE.  
DR SMART; SM00131; KU; 6.  
DR SM02083; WR1; 11.  
DR PROSITE; PS00080; BPTI\_KUNITZ\_1; 2.  
DR PROSITE; PS50079; BPTI\_KUNITZ\_2; 6.  
KW Serine protease inhibitor.  
SEQUENCE 1237 AA; 143867 MW; 6599F3D479A3A7DD CRC64;

Query Match 54.9%; Score 28; DB 5; Length 1297;  
Best Local Similarity 23.5%; Pred. No. 5.8;  
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=93785; PRELIMINARY; PRT; 2948 AA.  
AC Q93785; CREATED  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE P5414.1. PROTEIN.  
GN F5414.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
OC Rhabditidae; Peleriniae; Caenorhabditis.  
RN [1]  
SEQUENCE FROM N.A.  
RA Thomas K.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
SEQUENCE FROM N.A.  
RN MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
AC Connell M., Cooper J., Coulson A.,  
RA Bonfield J., Burton J., Copsey T., Dear S., Du Z.,  
RA Craxton M., Dear S., Du Z., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Latrell N.,  
RA Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA McMurray A., Mortimore B., Shownkeen R.,  
RA Parsons J., Percy C., Raffkin L., Roopra A.,  
RA Smalton N., Smith A., Sonnhammer E., Staden R.,  
RA Thierry-Mieg J., Thomas K., Vaughan K.,  
RA Watson A., Weinstock L., Wilkins-Sprott J., Wohldman P.;  
RT a 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RN [3]  
SEQUENCE FROM N.A.  
RX MEDLINE=9065613; PubMed=9851916; -.  
DR InterPro: IPR00400; WD40; 6.  
DR Pfam; PF00400; WD40; 6.  
DR SMART; SM00320; WD40; 6.  
DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
DR PROSITE; PS50088; WD\_REPEATS\_2; 2.  
DR PROSITE; PS50394; WD\_REPEATS\_REGION; 1.  
KW Repeat; WD repeat.  
SQ SEQUENCE 2948 AA; 330689 MW; 199DC767D3B43448 CRC64;

Query Match 54.9%; Score 28; DB 5; Length 2948;  
Best Local Similarity 23.5%; Pred. No. 6.3;  
Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
RN [1]  
SEQUENCE FROM N.A.  
AC Q9N329; CREATED  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE HYPOTHETICAL PROTEIN Y59E9AL 5.  
GN Y59E9AL 5.  
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peleoderae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1] RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL\_N2;  
 RX MEDLINE=99065613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode *C. elegans*: a platform for investigating biology." The *C. elegans* Sequencing Consortium. ";  
 RL Science 282:2012-2018 (1998).  
 RN [2] RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL\_N2;  
 RA Waterston R.;  
 DR Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.  
 EMBL; ACD24838; AAF60319.1; -;  
 SEQUENCE 99 AA; 11325 MW; EB3CC5FB7DAECC CRC64;  
 SQ

Query Match 52.9%; Score 27; DB 5; Length 99;  
 Best Local Similarity 23.5%; Pred. No. 7.8;  
 Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2 CXXXXCXXXXCXXXXC 18  
 Db 78 CTSAASRCSCRSPCSCGC 94

RESULT 13  
 Q9N95 ID Q9N95 PRELIMINARY; PRT; 233 AA.  
 Q9N95: 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE NHR-25 (FRAGMENT).  
 GN NHR-25.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peleoderae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;

RN [1] RP SEQUENCE FROM N.A.  
 RC STRAIN=N2;  
 RX MEDLINE=20237592; PubMed=10772806;  
 RA Gissendanner C.R.; Sluder A.E.;  
 RT "hr-25, the Caenorhabditis elegans ortholog of *ftz-f1*, is required for epidermal and somatic gonad development.";  
 RL Dev. Biol. 221:259-272 (2000).  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -!- SIMILARITY: TO C4 TYPE STEROID RECEPTOR ZINC FINGER FAMILY.  
 DR EMBL; AFI79216; AAF67040.1; -;  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF00105; zf-C4; 1.  
 PRINTS; PR00047; STRODIFINGER.  
 SMART; SM00399; zf-C4; 1.  
 PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 KW DNA binding; Nuclear protein; Receptor; Transcription regulation;  
 KW Zinc-finger.  
 FT NON-TER 233 233  
 SEQUENCE 233 AA; 26601 MW; 8387EA2B35646625 CRC64;

Query Match 52.9%; Score 27; DB 5; Length 233;  
 Best Local Similarity 23.5%; Pred. No. 8.6;  
 Matches 4; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2 CXXXXCXXXXCXXXXC 18  
 Db 54 CSAEANCHVDRICRKRC 700

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pflannoch C., Baldwin D.,  
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhanderi D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deig Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,  
 RA Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
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 DR HSSP; P15358; 1SNZ.  
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 SEQUENCE 441 AA; 46801 MW; 8021D0304127B97B CRC64;

Query Match 52.9%; Score 27; DB 5; Length 441;  
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 Db 214 CSSRDMCSSLNFCKVPC 230

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